

1652

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RAW SEQUENCE LISTING

DATE: 02/07/2002

PATENT APPLICATION: US/09/991,212A

TIME: 11:01:44

Input Set : N:\Crf3\RULE60\09991212A.raw

Output Set: N:\CRF3\02072002\I991212A.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: Lal, Preeti
6 Bandman, Olga
8 (ii) TITLE OF INVENTION: NOVEL HUMAN SODIUM-DEPENDENT
9 PHOSPHATE CO-TRANSPORTER
11 (iii) NUMBER OF SEQUENCES: 7
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
15 (B) STREET: 3174 Porter Drive
16 (C) CITY: Palo Alto
17 (D) STATE: CA
18 (E) COUNTRY: US
19 (F) ZIP: 94304
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Diskette
23 (B) COMPUTER: IBM Compatible
24 (C) OPERATING SYSTEM: DOS
25 (D) SOFTWARE: FastSEQ Version 2.0
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/09/991,212A
C--> 29 (B) FILING DATE: 16-Nov-2001
30 (C) CLASSIFICATION:
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: 09/391,958
34 (B) FILING DATE:
37 (viii) ATTORNEY/AGENT INFORMATION:
38 (A) NAME: Billings, Lucy J.
39 (B) REGISTRATION NUMBER: 36,749
40 (C) REFERENCE/DOCKET NUMBER: PF-0221 US
42 (ix) TELECOMMUNICATION INFORMATION:
43 (A) TELEPHONE: 415-855-0555
44 (B) TELEFAX: 415-845-4166
47 (2) INFORMATION FOR SEQ ID NO: 1:
49 (i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 401 amino acids
51 (B) TYPE: amino acid
52 (C) STRANDEDNESS: single
53 (D) TOPOLOGY: linear
55 (vii) IMMEDIATE SOURCE:
56 (A) LIBRARY: BRAITUT02
57 (B) CLONE: 754412
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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61 Met Gln Val Asp Glu Thr Leu Ile Pro Arg Lys Val Pro Ser Leu Cys
62 1 5 10 15
63 Ser Ala Arg Tyr Gly Ile Ala Leu Val Leu His Phe Cys Asn Phe Thr
64 20 25 30
65 Thr Ile Ala Gln Asn Val Ile Met Asn Ile Thr Met Val Ala Met Val
66 35 40 45
67 Asn Ser Thr Ser Pro Gln Ser Gln Leu Asn Asp Ser Ser Glu Val Leu
68 50 55 60
69 Pro Val Asp Ser Phe Gly Gly Leu Ser Lys Ala Pro Lys Ser Leu Pro
70 65 70 75 80
71 Ala Lys Ser Ser Ile Leu Gly Gly Gln Phe Ala Ile Trp Glu Arg Trp
72 85 90 95
73 Gly Pro Pro Gln Glu Arg Ser Arg Leu Cys Ser Ile Ala Leu Ser Gly
74 100 105 110
75 Met Leu Leu Gly Cys Phe Thr Ala Ile Leu Ile Gly Gly Phe Ile Ser
76 115 120 125
77 Glu Thr Leu Gly Trp Pro Phe Val Phe Tyr Ile Phe Gly Gly Val Gly
78 130 135 140
79 Cys Val Cys Cys Leu Leu Trp Phe Val Val Ile Tyr Asp Asp Pro Val
80 145 150 155 160
81 Ser Tyr Pro Trp Ile Ser Thr Ser Glu Lys Glu Tyr Ile Ile Ser Ser
82 165 170 175
83 Leu Lys Gln Gln Val Gly Ser Ser Lys Gln Pro Leu Pro Ile Lys Ala
84 180 185 190
85 Met Leu Arg Ser Leu Pro Ile Trp Ser Ile Cys Leu Gly Cys Phe Ser
86 195 200 205
87 His Gln Trp Leu Val Ser Thr Met Val Val Tyr Ile Pro Thr Tyr Ile
88 210 215 220
89 Ser Ser Val Tyr His Val Asn Ile Arg Asp Asn Gly Leu Leu Ser Ala
90 225 230 235 240
91 Leu Pro Phe Ile Val Ala Trp Val Ile Gly Met Val Gly Gly Tyr Leu
92 245 250 255
93 Ala Asp Phe Leu Leu Thr Lys Lys Phe Arg Leu Ile Thr Val Arg Lys
94 260 265 270
95 Ile Ala Thr Ile Leu Gly Ser Leu Pro Ser Ser Ala Leu Ile Val Ser
96 275 280 285
97 Leu Pro Tyr Leu Asn Ser Gly Tyr Ile Thr Ala Thr Ala Leu Leu Thr
98 290 295 300
99 Leu Ser Cys Gly Leu Ser Thr Leu Cys Gln Ser Gly Ile Tyr Ile Asn
100 305 310 315 320
101 Val Leu Asp Ile Ala Pro Arg Tyr Ser Ser Phe Leu Met Gly Ala Ser
102 325 330 335
103 Arg Gly Phe Ser Ser Ile Ala Pro Val Ile Val Pro Thr Val Ser Gly
104 340 345 350
105 Phe Leu Leu Ser Gln Asp Pro Glu Phe Gly Trp Arg Asn Val Phe Phe
106 355 360 365
107 Leu Leu Phe Ala Val Asn Leu Leu Gly Leu Leu Phe Tyr Leu Ile Phe
108 370 375 380
109 Gly Glu Ala Asp Val Gln Glu Trp Ala Lys Glu Arg Lys Leu Thr Arg

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110 385                      390                      395                      400
111 Leu
114 (2) INFORMATION FOR SEQ ID NO: 2:
116   (i) SEQUENCE CHARACTERISTICS:
117       (A) LENGTH: 1643 base pairs
118       (B) TYPE: nucleic acid
119       (C) STRANDEDNESS: single
120       (D) TOPOLOGY: linear
122   (vii) IMMEDIATE SOURCE:
123       (A) LIBRARY: BRAITUT02
124       (B) CLONE: 754412
126   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
128 AGAACGGTGA GGATGACCGA CGTATAGGCG AGAGCCTAGG TACGCCATGC CAGGTCACCG      60
129 GTCCGGCAAT TCCCGGGTCG ACCCACGCGT CCGCTTGGAG GGACGCTGGG TTCAACTTGA      120
130 AGCCCTTCCA CAGACATTAA GTCGGTGAAA ACCATTCACT AGGAGAGGAG AAACACAATG      180
131 GCCACCAAGA CAGAGTTGAG TCCACAGCA AGGGAGAGCA AGAACGCACA AGATATGCAA      240
132 GTGGATGAGA CACTGATCCC CAGGAAAGTT CCAAGTTTAT GTTCTGCTCG CTATGGAATA      300
133 GCCCTCGTCT TACATTTCTG CAATTTTACA ACGATAGCAC AAAATGTCAT CATGAACATC      360
134 ACCATGGTAG CCATGGTCAA CAGCACAAGC CCTCAATCCC AGCTCAATGA TTCCTCTGAG      420
135 GTGCTGCCTG TTGACTCATT TGGTGGCCTA AGTAAAGCCC CAAAGAGTCT TCCTGCAAAG      480
136 TCCTCAATAC TGCGGGGTCA GTTTGCAATT TGGGAAAGGT GGGGCCCTCC ACAAGAACGA      540
137 AGCAGACTCT GCAGCATTGC TTTATCAGGA ATGTTACTGG GATGCTTTAC TGCCATCCTC      600
138 ATAGGTGGCT TCATTAGTGA AACCCTTGGG TGGCCCTTTG TCTTCTATAT CTTTGGAGGT      660
139 GTTGGCTGTG TCTGCTGCCT TCTCTGGTTT GTTGTGATTT ATGATGACCC CGTTTCCTAT      720
140 CCATGGATAA GCACCTCAGA AAAAGAATAC ATCATATCCT CCTTGAAACA ACAGGTCGGG      780
141 TCTTCTAAGC AGCCTCTTCC CATCAAAGCT ATGCTCAGAT CTCTACCCAT TTGGTCCATA      840
142 TGTTTAGGCT GTTTCAGCCA TCAATGGTTA GTTAGCACAA TGGTTGTATA CATACCAACT      900
143 TACATCAGCT CTGTGTACCA TGTTAACATC AGAGACAATG GACTTCTATC TGCCCTTCCT      960
144 TTTATTGTTG CCTGGGTCAT AGGCATGGTG GGAGGCTATC TGGCAGATTT CCTTCTAACC     1020
145 AAAAAGTTTA GACTCATCAC TGTGAGGAAA ATTGCCACAA TTTTAGGAAG TCTCCCCTCT     1080
146 TCAGCACTCA TTGTGTCTCT GCCTTACCTC AATTCCGGCT ATATCACAGC AACTGCCTTG     1140
147 CTGACGCTCT CTTGCGGATT AAGCACATTG TGTCAGTCAG GGATTTATAT CAATGTCTTA     1200
148 GATATTGCTC CAAGGTATTC CAGTTTTTCTC ATGGGAGCAT CAAGAGGATT TTCGAGCATA     1260
149 GCACCTGTCA TTGTACCCAC TGTCAGCGGA TTTCTTCTTA GTCAGGACCC TGAGTTTGGG     1320
150 TGGAGGAATG TCTTCTTCTT GCTGTTTGCC GTTAACCTGT TAGGACTACT CTTCTACCTC     1380
151 ATATTTGGAG AAGCAGATGT CCAAGAATGG GCTAAAGAGA GAAAACCTCAC TCGTTTATGA     1440
152 AGTTATCCCA CCTTGGATGG AAAAGTCATT AGGCACCGTA TTGCATAAAA TAGAAGGCTT     1500
153 CCGTGATGAA AATACCAGTG AAAAGATTTT TTTTTCCTGT GGCTCTTTTC AATTATGAGA     1560
154 TCAGTTCATT ATTTTATTCA GACTTTTTTT TGAGAGAAAT GTAAGATGAA TAAAAATTCA     1620
155 AATAAAATGA TAACTAAGAA TGC
157 (2) INFORMATION FOR SEQ ID NO: 3:
159   (i) SEQUENCE CHARACTERISTICS:
160       (A) LENGTH: 467 amino acids
161       (B) TYPE: amino acid
162       (C) STRANDEDNESS: single
163       (D) TOPOLOGY: linear
165   (vii) IMMEDIATE SOURCE:
166       (A) LIBRARY: GenBank
167       (B) CLONE: 450532

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169 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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171 Met Gln Met Asp Asn Arg Leu Pro Pro Lys Val Pro Gly Phe Cys
172 1 5 10 15
173 Ser Phe Arg Tyr Gly Leu Ser Phe Leu Val His Cys Cys Asn Val Ile
174 20 25 30
175 Ile Thr Ala Gln Arg Ala Cys Leu Asn Leu Thr Met Val Val Met Val
176 35 40 45
177 Asn Ser Thr Asp Pro His Gly Leu Pro Asn Thr Ser Thr Lys Lys Leu
178 50 55 60
179 Leu Asp Asn Ile Lys Asn Pro Met Tyr Asn Trp Ser Pro Asp Ile Gln
180 65 70 75 80
181 Gly Ile Ile Leu Ser Ser Thr Ser Tyr Gly Val Ile Ile Ile Gln Val
182 85 90 95
183 Pro Val Gly Tyr Phe Ser Gly Ile Tyr Ser Thr Lys Lys Met Ile Gly
184 100 105 110
185 Phe Ala Leu Cys Leu Ser Ser Val Leu Ser Leu Leu Ile Pro Pro Ala
186 115 120 125
187 Ala Gly Ile Gly Val Ala Trp Val Val Val Cys Arg Ala Val Gln Gly
188 130 135 140
189 Ala Ala Gln Gly Ile Val Ala Thr Ala Gln Phe Glu Ile Tyr Val Lys
190 145 150 155 160
191 Trp Ala Pro Pro Leu Glu Arg Gly Arg Leu Thr Ser Met Ser Thr Ser
192 165 170 175
193 Gly Phe Leu Leu Gly Pro Phe Ile Val Leu Leu Val Thr Gly Val Ile
194 180 185 190
195 Cys Glu Ser Leu Gly Trp Pro Met Val Phe Tyr Ile Phe Gly Ala Cys
196 195 200 205
197 Gly Cys Ala Val Cys Leu Leu Trp Phe Val Leu Phe Tyr Asp Asp Pro
198 210 215 220
199 Lys Asp His Pro Cys Ile Ser Ile Ser Glu Lys Glu Tyr Ile Thr Ser
200 225 230 235 240
201 Ser Leu Val Gln Gln Val Ser Ser Ser Arg Gln Ser Leu Pro Ile Lys
202 245 250 255
203 Ala Ile Leu Lys Ser Leu Pro Val Trp Ala Ile Ser Ile Gly Ser Phe
204 260 265 270
205 Thr Phe Phe Trp Ser His Asn Ile Met Thr Leu Tyr Thr Pro Met Phe
206 275 280 285
207 Ile Asn Ser Met Leu His Val Asn Ile Lys Glu Asn Gly Phe Leu Ser
208 290 295 300
209 Ser Leu Pro Tyr Leu Phe Ala Trp Ile Cys Gly Asn Leu Ala Gly Gln
210 305 310 315 320
211 Leu Ser Asp Phe Phe Leu Thr Arg Asn Ile Leu Ser Val Ile Ala Val
212 325 330 335
213 Arg Lys Leu Phe Thr Ala Ala Gly Phe Leu Leu Pro Ala Ile Phe Gly
214 340 345 350
215 Val Cys Leu Pro Tyr Leu Ser Ser Thr Phe Tyr Ser Ile Val Ile Phe
216 355 360 365
217 Leu Ile Leu Ala Gly Ala Thr Gly Ser Phe Cys Leu Gly Gly Val Phe
218 370 375 380

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RAW SEQUENCE LISTING

DATE: 02/07/2002

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Input Set : N:\Crf3\RULE60\09991212A.raw

Output Set: N:\CRF3\02072002\I991212A.raw

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219 Ile Asn Gly Leu Asp Ile Ala Pro Arg Tyr Phe Gly Phe Ile Lys Ala
220 385          390          395          400
221 Cys Ser Thr Leu Thr Gly Met Ile Gly Gly Leu Ile Ala Ser Thr Leu
222          405          410          415
223 Thr Gly Leu Ile Leu Lys Gln Asp Pro Glu Ser Ala Trp Phe Lys Thr
224          420          425          430
225 Phe Ile Leu Met Ala Ala Ile Asn Val Thr Gly Leu Ile Phe Tyr Leu
226          435          440          445
227 Ile Val Ala Thr Ala Glu Ile Gln Asp Trp Ala Lys Glu Lys Gln His
228          450          455          460
229 Thr Arg Leu
230 465

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232 (2) INFORMATION FOR SEQ ID NO: 4:

234 (i) SEQUENCE CHARACTERISTICS:

235 (A) LENGTH: 560 amino acids

236 (B) TYPE: amino acid

237 (C) STRANDEDNESS: single

238 (D) TOPOLOGY: linear

240 (vii) IMMEDIATE SOURCE:

241 (A) LIBRARY: GenBank

242 (B) CLONE: 507415

244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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246 Met Glu Phe Arg Gln Glu Glu Phe Arg Lys Leu Ala Gly Arg Ala Leu
247 1          5          10          15
248 Gly Arg Leu His Arg Leu Leu Glu Lys Arg Gln Glu Gly Ala Glu Thr
249          20          25          30
250 Leu Glu Leu Ser Ala Asp Gly Arg Pro Val Thr Thr His Thr Arg Asp
251          35          40          45
252 Pro Pro Val Val Asp Cys Thr Cys Phe Gly Leu Pro Arg Arg Tyr Ile
253          50          55          60
254 Ile Ala Ile Met Ser Gly Leu Gly Phe Cys Ile Ser Phe Gly Ile Arg
255          65          70          75          80
256 Cys Asn Leu Gly Val Ala Ile Val Ser Met Val Asn Asn Ser Thr Thr
257          85          90          95
258 His Arg Gly Gly His Val Val Val Gln Lys Ala Gln Phe Asn Trp Asp
259          100         105         110
260 Pro Glu Thr Val Gly Leu Ile His Gly Ser Phe Phe Trp Gly Tyr Ile
261          115         120         125
262 Val Thr Gln Ile Pro Gly Gly Phe Ile Cys Gln Lys Phe Ala Ala Asn
263          130         135         140
264 Arg Val Phe Gly Phe Ala Ile Val Ala Thr Ser Thr Leu Asn Met Leu
265          145         150         155         160
266 Ile Pro Ser Ala Ala Arg Val His Tyr Gly Cys Val Ile Phe Val Arg
267          165         170         175
268 Ile Leu Gln Gly Leu Val Glu Gly Val Thr Tyr Pro Ala Cys His Gly
269          180         185         190
270 Ile Trp Ser Lys Trp Ala Pro Pro Leu Glu Arg Ser Arg Leu Ala Thr
271          195         200         205
272 Thr Ala Phe Cys Gly Ser Tyr Ala Gly Ala Val Val Ala Met Pro Leu

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VERIFICATION SUMMARY

DATE: 02/07/2002

PATENT APPLICATION: US/09/991,212A

TIME: 11:01:45

Input Set : N:\Crf3\RULE60\09991212A.raw

Output Set: N:\CRF3\02072002\I991212A.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]